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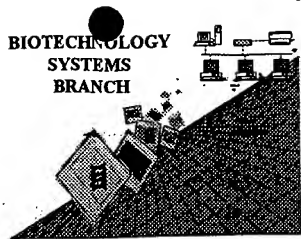
BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/202,104_

Source: _1647_

Date Processed by STIC: _7/31/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

 FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/202,104_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                                    This may occur if your file was retrieved in a word processor after creating it.
                                    Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                                    This may occur if your file was retrieved in a word processor after creating it.
                                    Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                    Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                    As per the rules, each n or Xaa can only represent a single residue.
                                    Please present the maximum number of each residue having variable length and
                                    indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                    sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                    to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
                                    sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                                    (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                    This sequence is intentionally skipped

                                    Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   **<210> sequence id number**
                                    <400> sequence id number
                                    000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
          (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
          (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
          (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                                    Please explain source of genetic material in <220> to <223> section.
                                    (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
                                    file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                    Instead, please use "File Manager" or any other means to copy file to floppy disk.

1647

RAW SE_JENCE LISTING   DA\E: 08/07/2000
PATENT APPLICATION: ·US/09/202,104   TIME: 20:15:31

Input Set : A:\3890us1.app
Output Set: N:\CRF3\08072000\I202104.raw

Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: van Leengoed, Leonardus Adrianus Maria Govardus
 4         Hoebe, Kasper Hubertus Nicolaas
 5         Meloen, Robert Hans
 7 <120> TITLE OF INVENTION: IL-6 and IL-6 receptor derived peptide having IL-6
 8         antagonistic or agonistic activity
10 <130> FILE REFERENCE: 2183-3890us
12 <140> CURRENT APPLICATION NUMBER: 09/202,104
13 <141> CURRENT FILING DATE: 1999-04-30
15 <150> PRIOR APPLICATION NUMBER: EP 96201720.8
16 <151> PRIOR FILING DATE: 1996-06-20
18 <150> PRIOR APPLICATION NUMBER: PCT/NL97/00345
19 <151> PRIOR FILING DATE: 1997-06-19
21 <160> NUMBER OF SEQ ID NOS: 19
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
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27 <212> TYPE: PRT
28 <213> ORGANISM: Unknown Organism
30 <220> FEATURE:
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63 Arg Gln Met
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 15
69 <212> TYPE: PRT
70 <213> ORGANISM: Unknown Organism
72 <220> FEATURE:
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(handwritten annotations: globel / invalid response — see circled portion / Item 12 on Error summary sheet)

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                    RAW SEQUENCE LISTING              DATE: 08/07/2000
                    PATENT APPLICATION:   US/09/202,104    TIME: 20:15:31

                    Input Set : A:\3890us1.app
                    Output Set: N:\CRF3\08072000\I202104.raw

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82 <212> TYPE: PRT
83 <213> ORGANISM: Unknown Organism
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Description of Unknown Organism PEPTIDE
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93              20
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101 <220> FEATURE:
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106   1             5                   10                  15
108 Phe Gln Gly Cys
109             20
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114 <212> TYPE: PRT
115 <213> ORGANISM: Unknown Organism
117 <220> FEATURE:
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125             20                  25
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130 <212> TYPE: PRT
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138   1             5                   10                  15
140 Lys Ala Lys Arg Asp Thr Pro Thr Ser
141             20                  25
144 <210> SEQ ID NO: 9
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                RAW SEQUENCE LISTING              DATE: 08/07/2000
                PATENT APPLICATION:  US/09/202,104  TIME: 20:15:31

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                Output Set: N:\CRF3\08072000\I202104.raw

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186              20                  25
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199  1                   5                  10                  15
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202              20                  25                  30
204 Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys
205          35                  40                  45
207 Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu
208          50                  55                  60
210 Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe
211  65                  70                  75                  80
213 Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe
214              85                  90                  95
216 Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu
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              RAW SEQUENCE LISTING                    DATE: 08/07/2000
              PATENT APPLICATION:  US/09/202,104      TIME: 20:15:31

              Input Set : A:\3890usl.app
              Output Set: N:\CRF3\08072000\I202104.raw

217             100                 105                 110
219 Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu
220         115                 120                 125
222 Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr
223         130                 135                 140
225 Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu
226 145                 150                 155                 160
228 Gln Asp Met Thr Thr His Leu Ile Leu Ile Arg Ser Phe Lys Glu Phe
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231 Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
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258         20                 25                 30
260 Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
261         35                 40                 45
263 Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Xaa Lys Phe Ser Cys
264         50                 55                 60
266 Xaa Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
267 65                  70                 75                 80
269 Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
270                 85                 90                 95
272 Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
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289   1                 5                 10                 15
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292             20              25                  30
294 Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys
295         35              40                  45
297 Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr
298     50              55                  60
300 Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu
301 65              70                  75                  80
303 Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val
304             85                  90                  95
306 Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn
307             100             105
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357 <400> SEQUENCE: 18
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362 <210> SEQ ID NO: 19
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please correct Seg19 if same even exist (handwritten note)

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/202,104

DATE: 08/07/2000
TIME: 20:15:32

Input Set : A:\3890us1.app
Output Set: N:\CRF3\08072000\I202104.raw

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L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13